



#9

1

SEQUENCE LISTING

<110> HIATT, ANDREW C.
HEIN, MICH B.

<120> METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
PROTECTION PROTEINS IN PLANTS AND THEIR USE

<130> EPI3002E

<140> 09/982,107

<141> 2001-10-16

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<170> PatentIn Ver. 2.1

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Phe Gly Ala Asn Asp Asn Met Gly Ala Ser Ser Ile Thr Gln Glu Thr	
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Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe
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Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp
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Gly Tyr Val Ser Asp Asp Tyr Val Gly Arg Ala Asn Leu Thr Asn Phe
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Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu
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Asn Phe Asp Val Ser Leu Glu Val Ser Gln Asp Pro Ala Gln Ala Ser
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His Ala His Val Tyr Thr Ile Asp Leu Gly Arg Thr Val Thr Ile Asn
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Cys Pro Phe Thr Arg Ala Asn Ser Glu Lys Arg Lys Ser Leu Cys Lys
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Asn Ile Asp Leu Gln Val Leu Glu Pro Glu Pro Glu Leu Val Tyr Gly	
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Cys	His	Phe	Pro	Cys	Lys	Phe	Tyr	Ser	Phe	Glu	Lys	Tyr	Trp	Cys	Lys	485	490	495	
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Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val	
655 660 665	
cga cat cgg aag aat gta gac cgc atg tca atc agc agc tac agg aca	2125
Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr	
670 675 680	
gac att agc atg gga gac ttc agg aac tcc agg gat ttg gga ggc aat	2173
Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn	
685 690 695 700	
gac aac atg ggc gcc act cca gac aca caa gaa aca gtc ctc gaa gga	2221
Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly	
705 710 715	

aaa gat gaa ata gag act acc acc gag tgt acc acc gag cca gag gaa 2269
 Lys Asp Glu Ile Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu
 720 725 730

tcc aag aaa gca aaa agg tca tcc aag gag gaa gct gac atg gcc tac 2317
 Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr
 735 740 745

tca gca ttc ctg ttt cag tcc agc aca ata gct gcg cag gtc cat gat 2365
 Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp
 750 755 760

ggt ccc cag gaa gcc tag gcagtgtga ccacctaccc ctgcctgtga 2413
 Gly Pro Gln Glu Ala
 765

caatcaactt gagaatcaca ttgatccact cgcagccac cctcgcccat caccaggct 2473
 ctccctcct gttctcagag gtgtgctggt tctccctca gtcgtggaag cctggcctac 2533
 ttatgcctgt ttaggagaga gcgtgaggag ttctttttgc tgttaaagag taagggtgaa 2593
 atgagttgag cccaagaggt gtctctgaga gacgaggggt cagagcaggg gctcatttca 2653
 ggaggaagag ccatttgaag cctctttata cacatatgct aggatgtcag gatagctctt 2713
 ctctccatc tctcctttct tctcttcttg attcagacaa cagatccgaa aactcactag 2773
 gcttcgggtg tctactaaat gctgagagtc aggccacagc ctttctataa acatcactgg 2833
 aagagacacc acctcgcccc agattctgtc ttttcctaa gctatcaatc attaccgggg 2893
 attccctttg cctctgcacc tcataggcaa caaaagaaac ataagtcctg cagtctaagg 2953
 cataccaag ccataagggc accacgagac tcagatgaga agagattttt ctccagagta 3013
 ctcagtgaga tagactagt tcaagccaga tggggcaact cctggctctt ggctggggac 3073
 ttgtcttcaa gatctctgct cttattagag aaagaacttt agcatgagga aaagtaagag 3133
 aaaacaagtt acatgggcat ggtggtgtgc tctgcaatc ccaatattaa gaggttaaaa 3193
 aataggacca gaagtttaaa gtaatccttg gctacctagt gagtgttaagg ccagcctgga 3253
 atcaataaga gttggt 3269

<210> 10
 <211> 769
 <212> PRT
 <213> Rattus sp.

<400> 10
 Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val
 1 5 10 15
 Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val Ser Ser Ile Glu
 20 25 30

Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
 35 40 45
 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys
 50 55 60
 Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
 65 70 75 80
 Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn
 85 90 95
 Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu
 100 105 110
 Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser
 115 120 125
 Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile
 130 135 140
 Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His
 145 150 155 160
 Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val
 165 170 175
 Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile
 180 185 190
 Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr Val Asn Ile Ser
 195 200 205
 His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys Gln Ala Gly Glu
 210 215 220
 Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln Val Leu Glu Pro
 225 230 235 240
 Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu
 245 250 255
 Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys Tyr Leu Cys Arg
 260 265 270
 Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg
 275 280 285
 Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro Arg Asp Asp Asn
 290 295 300
 Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly
 305 310 315 320
 His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp
 325 330 335

Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro
 340 345 350
 Asn Ser Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile
 355 360 365
 Val Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys
 370 375 380
 His Trp Glu Ala Asp Glu Asn Gly Arg Cys Pro Val Leu Val Gly Thr
 385 390 395 400
 Gln Ala Leu Val Gln Glu Gly Tyr Glu Gly Arg Leu Ala Leu Phe Asp
 405 410 415
 Gln Pro Gly Ser Gly Ala Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr
 420 425 430
 Gln Asp Ser Gly Phe Tyr Trp Cys Leu Thr Asp Gly Asp Ser Arg Trp
 435 440 445
 Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Lys Lys Pro Asp
 450 455 460
 Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Ile Gly Glu Thr Phe
 465 470 475 480
 Thr Ile Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr
 485 490 495
 Trp Cys Lys Trp Ser Asn Asp Gly Cys His Ile Leu Pro Ser His Asp
 500 505 510
 Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Ile
 515 520 525
 Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr
 530 535 540
 Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile
 545 550 555 560
 Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro
 565 570 575
 Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Glu Ala Met
 580 585 590
 Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg
 595 600 605
 Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln
 610 615 620
 Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly
 625 630 635 640

Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
 645 650 655
 Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
 660 665 670
 Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
 675 680 685
 Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
 690 695 700
 Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
 705 710 715 720
 Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
 725 730 735
 Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
 740 745 750
 Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
 755 760 765
 Ala

<210> 11
 <211> 322
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Guy's 13 Kappa

<220>
 <221> CDS
 <222> (8)..(322)

<400> 11
 ctcgagc gac att gtg atg acc cag tct cca gca atc atg tct gca tct 49
 Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
 1 5 10
 cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt gta agt 97
 Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
 15 20 25 30
 tac atg cac tgg ttc cag cag aag cca ggc act tct ccc aaa ctc tgg 145
 Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp
 35 40 45
 ctt tat agc aca tcc aac ctg gct tct gga gtc cct gct cgc ttc agt 193
 Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 50 55 60

ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga atg gag 241
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu
 65 70 75

gct gaa gat gct gcc act tat tac tgc cat caa agg act agt tac ccg 289
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro
 80 85 90

tac acg ttc gga ggg ggg acc aag ctg gaa ata 322
 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 95 100 105

<210> 12

<211> 105

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Guy's 13 Kappa

<400> 12

Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr
 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105

<210> 13

<211> 402

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Guy's 13 Gamma 1

<220>

<221> CDS

<222> (7)..(402)

<400> 13

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ctcgag atg gaa tgg acc tgg gtt ttt ctc ttc ctc ctg tca gga act 48
      Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr
        1             5             10

gca ggc gtc cac tct ggg gtc cag ctt cag cag tca gga cct gac ctg 96
Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu
  15             20             25             30

gtg aaa cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga tac 144
Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
              35             40             45

aca ttc act gac tac aac ata cac tgg gtg aag cag agc cgt gga aag 192
Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys
              50             55             60

agc ctt gag tgg att gga tat att tat cct tac aat ggt aat act tac 240
Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr
              65             70             75

tac aac cag aag ttc aag aac aag gcc aca ttg act gta gac aat tcc 288
Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser
              80             85             90

tcc acc tca gcc tac atg gag ctc cgc agc ctg aca tct gag gac tct 336
Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
  95             100            105            110

gca gtc tat tac tgt gca acc tac ttt gac tac tgg ggc caa ggc acc 384
Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
              115            120            125

act ctc aca gtc tcc tca 402
Thr Leu Thr Val Ser Ser
              130

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<210> 14

<211> 132

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Guy's 13 Gamma 1

<400> 14

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Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
  1             5             10             15

Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys
              20             25             30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
              35             40             45

Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu
  50             55             60

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Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr
 85 90 95
 Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu
 115 120 125
 Thr Val Ser Ser
 130

<210> 15
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 15
 accagatcta tggaatggac ctgggttttt c

31

<210> 16
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 16
 cccaagcttg gtttttgaga tggttttctc

30

<210> 17
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 17
 gataagcttg gtctactcc tcctcctct a

31

<210> 18
 <211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

aatctcgagt cagtagcaga tgccatctcc

30

<210> 19

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19

ggaaagcttt gtacatatgc aaggcttaca

30